

PTO/PCT Rec'd 09 AUG 2002

PATENT #4.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:
Irina Caminschi, et al.

Serial No.: 10/070,982

Filed: March 8, 2002

For: DENDRITIC CELL MEMBRANE
PROTEIN FIRE

Group Art Unit: Unknown

Examiner: Unknown

Atty. Dkt. No.: FBRC:011US

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SECOND PRELIMINARY AMENDMENT

BOX PCT
Commissioner for Patents
Washington, D.C. 20231

Sir:

Please amend the above-identified patent application as follows:

AMENDMENT

In the specification:

Please insert as the first paragraph of the specification the following paragraph:

This is a U.S. National Application under 35 U.S.C. § 371 of International Application

No. PCT/AU00/01083 filed on September 11, 2000, which claims the benefit of priority to AU
PQ 2728 filed on September 9, 1999.

In the claims:

Please amend claim 1 as follows:

10/16/2002 SANHED1 0000006 10070982

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406.00 OP

25146561.1

1. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1 or a functional fragment thereof or an amino acid sequence having at least 50% identity to the amino acid sequence of SEQ ID NO:1 or a functional fragment thereof.

Please add the following new claims:

27. (New) The isolated polypeptide of claim 1, wherein the amino acid sequence has at least 50% identity to the amino acid sequence of SEQ ID NO: 1.
28. (New) The isolated polypeptide of claim 27, wherein the amino acid sequence has at least 70% identity to the amino acid sequence of SEQ ID NO: 1.
29. (New) The isolated polypeptide of claim 27, wherein the amino acid sequence has at least 80% identity to the amino acid sequence of SEQ ID NO: 1.
30. (New) The isolated polypeptide of claim 27, wherein the amino acid sequence has at least 90% identity to the amino acid sequence of SEQ ID NO: 1.
31. (New) An isolated polypeptide comprising the amino acid sequence of SEQ ID NO:2 or a functional fragment thereof or an amino acid sequence having at least 50% identity to the amino acid sequence of SEQ ID NO:2 or a functional fragment thereof.
32. (New) The isolated polypeptide of claim 31, wherein the amino acid sequence has at least 50% identity to the amino acid sequence of SEQ ID NO: 2.
33. (New) The isolated polypeptide of claim 32, wherein the amino acid sequence has at least 70% identity to the amino acid sequence of SEQ ID NO: 2.
34. (New) The isolated polypeptide of claim 32, wherein the amino acid sequence has at least 80% identity to the amino acid sequence of SEQ ID NO: 2.
35. (New) The isolated polypeptide of claim 32, wherein the amino acid sequence has at least 90% identity to the amino acid sequence of SEQ ID NO: 2.

36. (New) An isolated ligand, wherein the ligand interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2.
37. (New) The isolated ligand of claim 36, wherein the functional fragment has at least 50% identity to the amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.
38. (New) The isolated ligand of claim 36, wherein the functional fragment has at least 70% identity to the amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.
39. (New) The isolated ligand of claim 36, wherein the functional fragment has at least 80% identity to the amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.
40. (New) The isolated ligand of claim 36, wherein the functional fragment has at least 90% identity to the amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.
41. (New) The isolated ligand of claim 36, wherein the functional fragment has the amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.
42. (New) The isolated ligand of claim 36, wherein the ligand is an antibody.
43. (New) The isolated ligand of claim 42, wherein the ligand is the binding portion of the antibody.
44. (New) An isolated nucleic acid molecule comprising the sequence of SEQ ID NO:3, a sequence having at least 60% identity to the sequence of SEQ ID NO:3, a sequence which hybridizes to the sequence of SEQ ID NO:3 under stringent conditions, or a sequence encoding a functional analogue of a polypeptide of SEQ ID NO:1.
45. (New) The isolated nucleic acid molecule of claim 44, wherein the nucleic acid molecule comprises a sequence of at least 60% identity with the sequence of SEQ ID NO:3.
46. (New) The isolated nucleic acid molecule of claim 45, wherein the nucleic acid molecule comprises a sequence of at least 70% identity with the sequence of SEQ ID NO:3.
47. (New) The isolated nucleic acid molecule of claim 45, wherein the nucleic acid molecule comprises a sequence of at least 80% identity with the sequence of SEQ ID NO:3.

48. (New) The isolated nucleic acid molecule of claim 45, wherein the nucleic acid molecule comprises a sequence of at least 90% identity with the sequence of SEQ ID NO:3.

49. (New) An isolated nucleic acid molecule comprising the sequence of SEQ ID NO:4, a sequence having at least 60% identity to the sequence of SEQ ID NO:, a sequence which hybridizes to the sequence of SEQ ID NO:4 under stringent conditions, or a sequence encoding a functional analogue of a polypeptide of SEQ ID NO:2.

50. (New) The isolated nucleic acid molecule of claim 49, wherein the nucleic acid molecule comprises a sequence of at least 60% identity with the sequence of SEQ ID NO:4.

51. (New) The isolated nucleic acid molecule of claim 50, wherein the nucleic acid molecule comprises a sequence of at least 70% identity with the sequence of SEQ ID NO:4.

52. (New) The isolated nucleic acid molecule of claim 50, wherein the nucleic acid molecule comprises a sequence of at least 80% identity with the sequence of SEQ ID NO:4.

53. (New) The isolated nucleic acid molecule of claim 50, wherein the nucleic acid molecule comprises a sequence of at least 90% identity with the sequence of SEQ ID NO:4.

54. (New) An isolated nucleic acid molecule encoding the binding region of a ligand, wherein the ligand interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2.

55. (New) The isolated nucleic acid molecule of claim 54, wherein the ligand is an antibody.

56. (New) A composition for use in raising or lowering an immune response in a subject comprising a ligand that interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2 and an antigen.

57. (New) The composition of claim 56, further comprising a carrier.

58. (New) The composition of claim 56, further comprising an adjuvant.

59. (New) The composition of claim 56, further comprising an adjuvant and a carrier.

60. (New) The composition of claim 56, wherein the antigen is associated with the ligand.

61. (New) The composition of claim 56, wherein the antigen is conjugated to the ligand.
62. (New) A composition for use in raising or lowering an immune response in a subject comprising a nucleic acid molecule and a carrier, wherein the nucleic acid molecule comprises a first sequence encoding a ligand that interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2 and a second sequence encoding an antigen.
63. (New) A method of screening a putative compound for immunological regulatory activity comprising;
- reacting the compound with a polypeptide comprising the amino acid sequence of SEQ ID NO:1 or a functional fragment thereof or an amino acid sequence having at least 50% identity to the amino acid sequence of SEQ ID NO:1 or a functional fragment thereof; and
 - measuring the interaction between the compound and the polypeptide.
64. (New) A method of isolating an antigen presenting cell from a biological sample comprising contacting the biological sample with a ligand, wherein the ligand interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2, to form a complex between the ligand and the antigen presenting cell and isolating the complex formed between the ligand and the antigen presenting cell from the biological sample.
65. (New) The method of claim 64, wherein the ligand is immobilized on a solid support.
66. (New) A method of immunizing a subject comprising:
- isolating antigen presenting cells from a fluid sample obtained from the subject, wherein the isolation involves contacting the fluid sample with a ligand that interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2;
 - exposing the cells isolated from step (a) to an antigen; and
 - reintroducing the cells from step (b) into the subject.

67. (New) The method of claim 66, further comprising the step of growing the antigen presenting cells *in vitro* after step (a).
68. A method of immunizing a subject comprising:
- (a) obtaining a fluid sample from the subject;
 - (b) isolating precursor cells from the fluid sample by contacting the fluid sample with a ligand that interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2;
 - (c) growing the cells isolated from step (a) *in vitro* such that they mature and differentiate to become antigen presenting cells;
 - (d) exposing the cells obtained in step (c) to an antigen; and
 - (e) reintroducing the cells from step (d) into the subject.
69. (New) A method of modulating an immune response in a subject comprising administering to the subject a ligand that interacts with a functional fragment of SEQ ID NO: 1 or SEQ ID NO: 2 such that the ligand binds to and inhibits the function of an antigen presenting cell.
70. (New) The method of claim 69, wherein the antigen presenting cell is a myeloid dendritic cell.
71. (New) The method of claim 69, further comprising the step of administering an antigen to the subject.
72. (New) The method of claim 71, wherein the antigen is administered after administration of the ligand.

REMARKS

I. State of the claims

Claims 1-26 were present in the PCT application and were filed with the application on March 8, 2002. Claims 2-26 were cancelled without prejudice or disclaimer in a First Preliminary Amendment filed concurrently with the application. Applicants expressly reserved the right to pursue claims to the subject matter of claims 2-26. Applicants add by the present amendment claims 27-72. Therefore, claims 1 and 27-72 are currently pending. No new matter is introduced by these amendments.

II. Conclusion

Examination of the amended claims is respectfully requested.

Respectfully submitted,



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Date: August 9, 2002

10/070982

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Express Mail Cert. No. EL794535315US
Date: March 8, 2002

PATENT

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
DO/EO/US RECEIVING OFFICE**

Applicants for DO/EO/US:

Irina CAMINSCHI, Stephane Alain
VANDENABEELE, Mark Dexter WRIGHT,
Kenneth Douglas SHORTMAN

Atty. Dkt. No.: FBRC:011/TMB

International Application No.: PCT/AU00/01083

International Filing Date: 11 September 2000

Title: DENDRITIC CELL MEMBRANE PROTEIN
FIRE

PRELIMINARY AMENDMENT

BOX PCT

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Please amend the above-identified patent application as follows:

AMENDMENT

In the claims:

Please cancel without prejudice or disclaimer claims 2-26.

REMARKS

I. State of the claims

Claims 1-26 were present in the PCT application and were filed herewith. Claims 2-26 have been cancelled without prejudice or disclaimer. Applicants expressly reserve the right to pursue claims to the subject matter of claims 2-26.

II. Conclusion

The claims have been amended to eliminate multiple dependencies. Examination of the amended claim is respectfully requested.

No fees are believed to be due in connection with the filing of this Preliminary Amendment; however, should any fees under 37 C.F.R §§ 1.16 to 1.21 be deemed necessary for any reason relating to the enclosed materials, the Commissioner is hereby authorized to deduct said fees from Fulbright & Jaworski Deposit Account No. 50-1212/10011874/TMB.

Respectfully submitted,



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Date: March 8, 2002

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Gly Asn Tyr Ser Cys Phe Cys Asn Pro Gly Phe Glu Ser Ser Ser Gly
 195 200 205

His Leu Ser Cys Gln Gly Leu Lys Ala Ser Cys Glu Asp Ile Asp Glu
 210 215 220

Cys	Thr	Glu	Met	Cys	Pro	Ile	Asn	Ser	Thr	Cys	Thr	Asn	Thr	Pro	Gly
225						230				235					240
Ser	Tyr	Phe	Cys	Thr	Cys	His	Pro	Gly	Phe	Ala	Pro	Ser	Ser	Gly	Gln
						245				250					255
Leu	Asn	Phe	Thr	Asp	Gln	Gly	Val	Glu	Cys	Arg	Asp	Ile	Asp	Glu	Cys
							260		265						270
Arg	Gln	Asp	Pro	Ser	Thr	Cys	Gly	Pro	Asn	Ser	Ile	Cys	Thr	Asn	Ala
								275		280					285
Leu	Gly	Ser	Tyr	Ser	Cys	Gly	Cys	Ile	Val	Gly	Phe	His	Pro	Asn	Pro
							290		295						300
Glu	Gly	Ser	Gln	Lys	Asp	Gly	Asn	Phe	Ser	Cys	Gln	Arg	Val	Leu	Phe
							305		310			315			320
Lys	Cys	Lys	Glu	Asp	Val	Ile	Pro	Asp	Asn	Lys	Gln	Ile	Gln	Gln	Cys
							325			330					335
Gln	Glu	Gly	Thr	Ala	Val	Lys	Pro	Ala	Tyr	Val	Ser	Phe	Cys	Ala	Gln
							340			345					350
Ile	Asn	Asn	Ile	Phe	Ser	Val	Leu	Asp	Lys	Val	Cys	Glu	Asn	Lys	Thr
							355		360						365
Thr	Val	Val	Ser	Leu	Lys	Asn	Thr	Thr	Glu	Ser	Phe	Val	Pro	Val	Leu
							370		375						380
Lys	Gln	Ile	Ser	Met	Trp	Thr	Lys	Phe	Thr	Lys	Glu	Glu	Thr	Ser	Ser
							385		390			395			400
Leu	Ala	Thr	Val	Phe	Leu	Glu	Ser	Val	Glu	Ser	Met	Thr	Leu	Ala	Ser
							405			410					415
Phe	Trp	Lys	Pro	Ser	Ala	Asn	Val	Thr	Pro	Ala	Val	Arg	Ala	Glu	Tyr
							420			425					430
Leu	Asp	Ile	Glu	Ser	Lys	Val	Ile	Asn	Lys	Glu	Cys	Ser	Glu	Glu	Asn
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Val	Thr	Leu	Asp	Leu	Val	Ala	Lys	Gly	Asp	Lys	Met	Lys	Ile	Gly	Cys
							450		455				460		
Ser	Thr	Ile	Glu	Glu	Ser	Glu	Ser	Thr	Glu	Thr	Thr	Gly	Val	Ala	Phe
								465			475				480
Val	Ser	Phe	Val	Gly	Met	Glu	Ser	Val	Leu	Asn	Glu	Arg	Phe	Phe	Gln
								485			490				495
Asp	His	Gln	Ala	Pro	Leu	Thr	Thr	Ser	Glu	Ile	Lys	Leu	Lys	Met	Asn
								500			505				510

Ser Arg Val Val Gly Gly Ile Met Thr Gly Glu Lys Lys Asp Gly Phe
515 520 525

Ser Asp Pro Ile Ile Tyr Thr Leu Glu Asn Val Gln Pro Lys Gln Lys
530 535 540

Phe Glu Arg Pro Ile Cys Val Ser Trp Ser Thr Asp Val Lys Gly Gly
545 550 555 560

Arg Trp Thr Ser Phe Gly Cys Val Ile Leu Glu Ala Ser Glu Thr Tyr
565 570 575

Thr Ile Cys Ser Cys Asn Gln Met Ala Asn Leu Ala Val Ile Met Ala
580 585 590

Ser Gly Glu Leu Thr Met Asp Phe Ser Leu Tyr Ile Ile Ser His Val
595 600 605

Gly Ile Ile Ile Ser Leu Val Cys Leu Val Leu Ala Ile Ala Thr Phe
610 615 620

Leu Leu Cys Arg Ser Ile Arg Asn His Asn Thr Tyr Leu His Leu His
625 630 635 640

Leu Cys Val Cys Leu Leu Leu Ala Lys Thr Leu Phe Leu Ala Gly Ile
645 650 655

His Lys Thr Asp Asn Lys Thr Gly Cys Ala Ile Ile Ala Gly Phe Leu
660 665 670

His Tyr Leu Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val
675 680 685

Ile Leu Phe Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser
690 695 700

Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu
705 710 715 720

Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr
725 730 735

Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp
740 745 750

Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu
755 760 765

Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn
770 775 780

Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala
785 790 795 800

Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe

165	170	175
Cys Val Thr Arg Asp Val Cys Pro Glu His Ala Thr Cys His Asn Thr 180	185	190
Leu Gly Ser Tyr Tyr Cys Thr Cys Asn Ser Gly Leu Glu Ser Ser Gly 195	200	205
Gly Gly Pro Met Phe Gln Gly Leu Asp Glu Ser Cys Glu Asp Val Asp 210	215	220
Glu Cys Ser Arg Asn Ser Thr Leu Cys Gly Pro Thr Phe Ile Cys Ile 225	230	235
Asn Thr Leu Gly Ser Tyr Ser Cys Ser Cys Pro Ala Gly Phe Ser Leu 245	250	255
Pro Thr Phe Gln Ile Leu Gly His Pro Ala Asp Gly Asn Cys Thr Asp 260	265	270
Ile Asp Glu Cys Asp Asp Thr Cys Pro Leu Asn Ser Ser Cys Thr Asn 275	280	285
Thr Ile Gly Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Ser Ser 290	295	300
Asn Gly Gln Leu Asn Phe Lys Asp Leu Glu Val Thr Cys Glu Asp Ile 305	310	315
Asp Glu Cys Thr Gln Asp Pro Leu Gln Cys Gly Leu Asn Ser Val Cys 325	330	335
Thr Asn Val Pro Gly Ser Tyr Ile Cys Gly Cys Leu Pro Asp Phe Gln 340	345	350
Met Asp Pro Glu Gly Ser Gln Gly Tyr Gly Asn Phe Asn Cys Lys Arg 355	360	365
Ile Leu Phe Lys Cys Lys Glu Asp Leu Ile Leu Gln Ser Glu Gln Ile 370	375	380
Gln Gln Cys Gln Ala Val Gln Gly Arg Asp Leu Gly Tyr Ala Ser Phe 385	390	395
Cys Thr Leu Val Asn Ala Thr Phe Thr Ile Leu Asp Asn Thr Cys Glu 405	410	415
Asn Lys Ser Ala Pro Val Ser Leu Gln Ser Ala Ala Thr Ser Val Ser 420	425	430
Leu Val Leu Glu Gln Ala Thr Thr Trp Phe Glu Leu Ser Lys Glu Glu 435	440	445
Thr Ser Thr Leu Gly Thr Ile Leu Leu Glu Thr Val Glu Ser Thr Met 450	455	460

Leu Ala Ala Leu Leu Ile Pro Ser Gly Asn Ala Ser Gln Met Ile Gln
 465 470 475 480

Thr Glu Tyr Leu Asp Ile Glu Ser Lys Val Ile Asn Glu Glu Cys Lys
 485 490 495

Glu Asn Glu Ser Ile Asn Leu Ala Ala Arg Gly Asp Lys Met Asn Val
 500 505 510

Gly Cys Phe Ile Ile Lys Glu Ser Val Ser Thr Gly Ala Pro Gly Val
 515 520 525

Ala Phe Val Ser Phe Ala His Met Glu Ser Val Leu Asn Glu Arg Phe
 530 535 540

Phe Glu Asp Gly Gln Ser Phe Arg Lys Leu Arg Met Asn Ser Arg Val
 545 550 555 560

Val Gly Gly Thr Val Thr Gly Glu Lys Lys Glu Asp Phe Ser Lys Pro
 565 570 575

Ile Ile Tyr Thr Leu Gln His Ile Gln Pro Lys Gln Lys Ser Glu Arg
 580 585 590

Pro Ile Cys Val Ser Trp Asn Thr Asp Val Glu Asp Gly Arg Trp Thr
 595 600 605

Pro Ser Gly Cys Glu Ile Val Glu Ala Ser Glu Thr His Thr Val Cys
 610 615 620

Ser Cys Asn Arg Met Ala Asn Leu Ala Ile Ile Met Ala Ser Gly Glu
 625 630 635 640

Leu Thr Met Glu Phe Ser Leu Tyr Ile Ile Ser His Val Gly Thr Val
 645 650 655

Ile Ser Leu Val Cys Leu Ala Leu Ala Ile Ala Thr Phe Leu Leu Cys
 660 665 670

Arg Ala Val Gln Asn His Asn Thr Tyr Met His Leu His Leu Cys Val
 675 680 685

Cys Leu Phe Leu Ala Lys Ile Leu Phe Leu Thr Gly Ile Asp Lys Thr
 690 695 700

Asp Asn Gln Thr Ala Cys Ala Ile Ile Ala Gly Phe Leu His Tyr Leu
 705 710 715 720

Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val Met Leu Phe
 725 730 735

Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser Ser Arg Asn
 740 745 750

Ile Lys Met Leu His Leu Cys Ala Phe Gly Tyr Gly Leu Pro Val Leu
755 760 765

Val Val Ile Ile Ser Ala Ser Val Gln Pro Arg Gly Tyr Gly Met His
770 775 780

Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp Ser Phe Leu
785 790 795 800

Gly Pro Val Cys Met Ile Ile Thr Ile Asn Ser Val Leu Leu Ala Trp
805 810 815

Thr Leu Trp Val Leu Arg Gln Lys Leu Cys Ser Val Ser Ser Glu Val
820 825 830

Ser Lys Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala Ile Ala Gln
835 840 845

Ile Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe Gln Ile Gly
850 855 860

Pro Leu Ala Ser Ile Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser Leu
865 870 875 880

Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn Arg Gln Val
885 890 895

Arg Asp Glu Tyr Lys Lys Leu Leu Thr Arg Lys Thr Asp Leu Ser Ser
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His Ser Gln Thr Ser Gly Ile Leu Leu Ser Ser Met Pro Ser Thr Ser
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Lys Met Gly
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<210> 7

<211> 740

<212> PRT

<213> Homo sapiens

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Asn Ser Ser Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe
35 40 45

Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp
50 55 60

Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser
 65 70 75 80

Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly
 85 90 95

Tyr Glu Pro Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn
 100 105 110

Thr Cys Gln Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser
 115 120 125

Thr Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys Arg Pro
 130 135 140

Gly Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp Thr Val
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Cys Glu Asp Met Thr Phe Ser Thr Trp Thr Pro Pro Pro Gly Val His
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Ser Gln Thr Leu Ser Arg Phe Phe Asp Lys Val Gln Asp Leu Gly Arg
 180 185 190

Asp Ser Lys Thr Ser Ser Ala Glu Val Thr Ile Gln Asn Val Ile Lys
 195 200 205

Leu Val Asp Glu Leu Met Glu Ala Pro Gly Asp Val Glu Ala Leu Ala
 210 215 220

Pro Pro Val Arg His Leu Ile Ala Thr Gln Leu Leu Ser Asn Leu Glu
 225 230 235 240

Asp Ile Met Arg Ile Leu Ala Lys Ser Leu Pro Lys Gly Pro Phe Thr
 245 250 255

Tyr Ile Ser Pro Ser Asn Thr Glu Leu Thr Leu Met Ile Gln Glu Arg
 260 265 270

Gly Asp Lys Asn Val Thr Met Gly Gln Ser Ser Ala Arg Met Lys Leu
 275 280 285

Asn Trp Ala Val Ala Ala Gly Ala Glu Asp Pro Gly Pro Ala Val Ala
 290 295 300

Gly Ile Leu Ser Ile Gln Asn Met Thr Thr Leu Leu Ala Asn Ala Ser
 305 310 315 320

Leu Asn Leu His Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu
 325 330 335

Ser Ser Ile Arg Gly Val Gln Leu Arg Arg Leu Ser Ala Val Asn Ser
 340 345 350

Ile Phe Leu Ser His Asn Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu

Phe Ala Phe Ser His Leu Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp
 370 375 380

Pro Pro Ala Lys Asp Val Met Pro Gly Pro Arg Gln Glu Leu Leu Cys
 385 390 395 400

Ala Phe Trp Lys Ser Asp Ser Asp Arg Gly Gly His Trp Ala Thr Glu
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Val Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys
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Ser His Leu Ser Ser Phe Thr Ile Leu Met Ala His Tyr Asp Val Glu
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Asp Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu
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Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile
 465 470 475 480

Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe
 485 490 495

Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gln
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Val Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe
 515 520 525

Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe
 530 535 540

Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu
 545 550 555 560

Cys Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala
 565 570 575

Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp
 580 585 590

Phe Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile
 595 600 605

Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr
 610 615 620

Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala
 625 630 635 640

Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys
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Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu
660 665 670

Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr
675 680 685

Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys
690 695 700

Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser
705 710 715 720

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725 730 735

Glu Ser Gly Ile
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<211> 30
<212> DNA
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cgcgaaagctt tcaatcttga catttctcat gg 32

<210> 10
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<220>
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gacgggatcc aatgagtgtc tactgaaaga attg 34

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primers

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accgaagtt tcagctcttg ttcacataac aatc

34

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<220>
<223> Description of Artificial Sequence: PCR primers

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30

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<223> Description of Artificial Sequence: PCR primers

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34

<210> 14
<211> 31
<212> DNA
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<400> 14
acacggatcc actttgggag tactgagtga a

31

<210> 15
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<400> 15
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<400> 16
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<210> 17
<211> 23
<212> DNA
<213> *Mus musculus*

<400> 17
gaaagtttgc ttctcaaaat cca 23

<210> 18
<211> 26
<212> DNA
<213> *Homo sapiens*

<400> 18
tgcctcattq caccctttgg tttcat 26

<210> 19
<211> 19
<212> DNA
<213> Homo sapiens

<400> 19
ccacaacaqc acccaactgt 19

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<210> 20
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<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: PCR primer

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<210> 21

<211> 33
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 21

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33

<210> 22

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 22

cgggatcc tcctatgggtt agagcc

26

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 23

cgggtaccac catgggaagc aggtgccttc tgc

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<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR primer

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<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR primer

<400> 25

cctttcctg gcccacct

SEQUENCE LISTING

<110> CAMINSCHI ET AL.

<120> DENDRITIC CELL MEMBRANE PROTEIN FIRE

<130> FBRC:0111US

<140> 10/070,982

<141> 2002-03-08

<150> PCT/AU00/01083

<151> 2000-09-11

<160> 25

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<213> Mus musculus

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Ile Trp Ser Ile Leu Gln Met Met Asn Ile Ser Ala Ser Cys Pro Gln
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Cys Asn Glu Asn Ala Ser Cys Phe Asn Ser Thr His Cys Val Cys Lys
35 40 45

Glu Gly Phe Trp Thr Gly Ser Glu Asn Arg Arg Ile Ile Glu Pro His
50 55 60

Glu Lys Cys Gln Asp Ile Asn Glu Cys Leu Leu Lys Glu Leu Val Cys
65 70 75 80

Lys Asp Val Ser Tyr Cys Arg Asn Lys Ile Gly Thr Tyr Ile Cys Ser
85 90 95

Cys Val Val Lys Tyr Pro Leu Phe Asn Trp Val Ala Gly Ile Ile Asn
100 105 110

Ile Asp His Pro Asp Cys Tyr Val Asn Lys Ser Lys Asn Thr Gly Ser
115 120 125

Lys Thr His Thr Leu Gly Val Leu Ser Glu Phe Lys Ser Lys Glu Glu
130 135 140

Val Ala Lys Gly Ala Thr Lys Leu Leu Arg Lys Val Glu His His Ile
145 150 155 160

Leu Asn Glu Asn Ser Asp Ile Pro Lys Lys Asp Glu Asn Pro Leu Leu
165 170 175

Asp Ile Val Tyr Glu Thr Lys Arg Cys Lys Thr Met Thr Leu Leu Glu
180 185 190

Ala Gly Asn Asn Thr Met Lys Val Asp Cys Thr Ser Gly Phe Lys Glu
195 200 205

His Asn Ser Gly Gly Glu Thr Ala Val Ala Phe Ile Ala Tyr Lys Ser
210 215 220

Leu Gly Asn Leu Leu Asn Gly Ser Phe Phe Ser Asn Glu Glu Gly Phe
225 230 235 240

Gln Glu Val Thr Leu Asn Ser His Ile Val Ser Gly Ala Ile Arg Ser
245 250 255

Glu Val Lys Pro Val Leu Ser Glu Pro Val Leu Leu Thr Leu Gln Asn
260 265 270

Ile Gln Pro Ile Asp Ser Arg Ala Glu His Leu Cys Val His Trp Glu
275 280 285

Gly Ser Glu Glu Gly Gly Ser Trp Ser Thr Lys Gly Cys Ser His Val
290 295 300

Tyr Thr Asn Asn Ser Tyr Thr Ile Cys Lys Cys Phe His Leu Ser Ser
305 310 315 320

Phe Ala Val Leu Met Ala Leu Pro His Glu Glu Asp Gly Val Leu Ser
325 330 335

Ala Leu Ser Val Ile Thr Tyr Val Gly Leu Ser Leu Ser Leu Leu Cys
340 345 350

Leu Phe Leu Ala Ala Ile Thr Phe Leu Leu Cys Arg Pro Ile Gln Asn
355 360 365

Thr Ser Thr Thr Leu His Leu Gln Leu Ser Ile Cys Leu Phe Leu Ala
370 375 380

Asp Leu Leu Phe Leu Thr Gly Ile Asn Arg Thr Lys Pro Lys Val Leu
385 390 395 400

Cys Ser Ile Ile Ala Gly Met Leu His Tyr Leu Tyr Leu Ala Ser Phe
405 410 415

Met Trp Met Phe Leu Glu Gly Leu His Leu Phe Leu Thr Val Ser Asn
420 425 430

Leu Lys Val Ala Asn Tyr Ser Asn Ser Gly Arg Phe Lys Lys Arg Phe
435 440 445

Met Tyr Pro Val Gly Tyr Gly Leu Pro Ala Phe Ile Val Ala Val Ser
450 455 460

Ala Ile Ala Gly His Lys Asn Tyr Gly Thr His Asn His Cys Trp Leu
465 470 475 480

Ser Leu His Arg Gly Phe Ile Trp Ser Phe Leu Gly Pro Ala Ala Ala
485 490 495

Ile Ile Leu Ile Asn Leu Val Phe Tyr Phe Leu Ile Ile Trp Ile Leu
500 505 510

Arg Ser Lys Leu Ser Ser Leu Asn Lys Glu Val Ser Thr Leu Gln Asp
515 520 525

Thr Lys Val Met Thr Phe Lys Ala Ile Val Gln Leu Phe Val Leu Gly
530 535 540

Cys Ser Trp Gly Ile Gly Leu Phe Ile Phe Ile Glu Val Gly Lys Thr
545 550 555 560

Val Arg Leu Ile Val Ala Tyr Leu Phe Thr Ile Ile Asn Val Leu Gln
565 570 575

Gly Val Leu Ile Phe Met Val His Cys Leu Leu Asn Arg Gln Val Arg
580 585 590

Met Glu Tyr Lys Lys Trp Phe His Arg Leu Arg Lys Glu Val Glu Ser
595 600 605

Glu Ser Thr Glu Val Ser His Ser Thr Thr His Thr Lys Met Gly Leu
610 615 620

Ser Leu Asn Leu Glu Asn Phe Cys Pro Thr Gly Asn Leu His Asp Pro
625 630 635 640

Ser Asp Ser Ile Leu Pro Ser Thr Glu Val Ala Gly Val Tyr Leu Ser
645 650 655

Thr Pro Arg Ser His Met Gly Ala Glu Asp Val Asn Ser Gly Thr His
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Ala Tyr Trp Ser Arg Thr Ile Ser Asp
675 680

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Phe His Asp Ser Ser Glu Lys Cys Glu Asp Ile Asn Glu Cys Glu Thr
35 40 45

Gly Leu Ala Lys Cys Lys Tyr Lys Ala Tyr Cys Arg Asn Lys Val Gly
50 55 60

Gly Tyr Ile Cys Ser Cys Leu Val Lys Tyr Thr Leu Phe Asn Phe Leu
65 70 75 80

Ala Gly Ile Ile Asp Tyr Asp His Pro Asp Cys Tyr Glu Asn Asn Ser
85 90 95

Gln Gly Thr Thr Gln Ser Asn Val Asp Ile Trp Glu Asn Leu Arg Arg
100 105 110

Asn Gly Ser Arg Glu Asp Phe Ala Arg Arg Ala Thr Gln Leu Ile Gln
115 120 125

Ser Val Glu Leu Ser Ile Trp Asn Ala Ser Phe Ala Ser Pro Gly Lys
130 135 140

Gly Gln Ile Ser Glu Phe Asp Ile Val Tyr Glu Thr Lys Arg Cys Asn
145 150 155 160

Glu Thr Arg Glu Asn Ala Phe Leu Glu Ala Gly Asn Asn Thr Met Asp
165 170 175

Ile Asn Cys Ala Asp Ala Leu Lys Gly Asn Leu Arg Glu Ser Thr Ala
180 185 190

Val Ala Leu Ile Thr Tyr Gln Ser Leu Gly Asp Ile Leu Asn Ala Ser
195 200 205

Phe Phe Ser Lys Arg Lys Gly Met Gln Glu Val Lys Leu Asn Ser Tyr
210 215 220

Val Val Ser Gly Thr Val Gly Leu Lys Glu Lys Ile Ser Leu Ser Glu
225 230 235 240

Pro Val Phe Leu Thr Phe Arg His Asn Gln Pro Gly Asp Lys Arg Thr
245 250 255

Lys His Ile Cys Val Tyr Trp Glu Gly Ser Glu Gly Gly Arg Trp Ser
260 265 270

Thr Glu Gly Cys Ser His Val His Ser Asn Gly Ser Tyr Thr Lys Cys
275 280 285

Lys Cys Phe His Leu Ser Ser Phe Ala Val Leu Val Ala Leu Ala Pro
290 295 300

Lys Glu Asp Pro Val Leu Thr Val Ile Thr Gln Val Gly Leu Thr Ile
305 310 315 320

Ser Leu Leu Cys Leu Phe Leu Ala Ile Leu Thr Phe Leu Leu Cys Arg
325 330 335

Pro Ile Gln Asn Thr Ser Thr Ser Leu His Leu Glu Leu Ser Leu Cys
340 345 350

Leu Phe Leu Ala His Leu Leu Phe Leu Thr Gly Ile Asn Arg Thr Glu
355 360 365

Pro Glu Val Leu Cys Ser Ile Ile Ala Gly Leu Leu His Phe Leu Tyr
370 375 380

Leu Ala Cys Phe Thr Trp Met Leu Leu Glu Gly Leu His Leu Phe Leu
385 390 395 400

Thr Val Arg Asn Leu Lys Val Ala Asn Tyr Thr Ser Thr Gly Arg Phe
405 410 415

Lys Lys Arg Phe Met Tyr Pro Val Gly Tyr Gly Ile Pro Ala Val Ile
420 425 430

Ile Ala Val Ser Ala Ile Val Gly Pro Gln Asn Tyr Gly Thr Phe Thr
435 440 445

His Cys Trp Leu Lys Leu Asp Lys Gly Phe Ile Trp Ser Phe Met Gly
450 455 460

Pro Val Ala Val Ile Ile Leu Ile Asn Leu Val Phe Tyr Phe Gln Val
465 470 475 480

Leu Trp Ile Leu Arg Ser Lys Leu Ser Ser Leu Asn Lys Glu Val Ser
485 490 495

Thr Ile Gln Asp Thr Arg Val Met Thr Phe Lys Ala Ile Ser Gln Leu
500 505 510

Phe Ile Leu Gly Cys Ser Trp Gly Leu Gly Phe Phe Met Val Glu Glu
515 520 525

Val Gly Lys Thr Ile Gly Ser Ile Ile Ala Tyr Ser Phe Thr Ile Ile
530 535 540

Asn Thr Leu Gln Gly Val Leu Leu Phe Val Val His Cys Leu Leu Asn
545 550 555 560

Arg Gln Val Arg Met Glu Tyr Lys Lys Trp Phe Ser Gly Met Arg Lys
565 570 575

Gly Val Glu Thr Glu Ser Thr Glu Met Ser Arg Ser Thr Thr Gln Thr
580 585 590

Lys Thr Glu Glu Val Gly Lys Ser Ser Glu Ile Phe His Lys Gly Gly
595 600 605

Thr Ala Ser Ser Ser Ala Glu Ser Thr Lys Gln Pro Gln Pro Gln Val
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<213> Mus musculus

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<213> Homo sapiens
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<212> PRT
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35 40 45
Asn Thr Val Asp Ser Tyr Tyr Cys Thr Cys Lys Gln Gly Phe Leu Ser
50 55 60
Ser Asn Gly Gln Asn His Phe Lys Asp Pro Gly Val Arg Cys Lys Asp
65 70 75 80
Ile Asp Glu Cys Ser Gln Ser Pro Gln Pro Cys Gly Pro Asn Ser Ser
85 90 95
Cys Lys Asn Leu Ser Gly Arg Tyr Lys Cys Ser Cys Leu Asp Gly Phe
100 105 110
Ser Ser Pro Thr Gly Asn Asp Trp Val Pro Gly Lys Pro Gly Asn Phe
115 120 125
Ser Cys Thr Asp Ile Asn Glu Cys Leu Thr Ser Arg Val Cys Pro Glu
130 135 140
His Ser Asp Cys Val Asn Ser Met Gly Ser Tyr Ser Cys Ser Cys Gln
145 150 155 160
Val Gly Phe Ile Ser Arg Asn Ser Thr Cys Glu Asp Val Asn Glu Cys
165 170 175
Ala Asp Pro Arg Ala Cys Pro Glu His Ala Thr Cys Asn Asn Thr Val
180 185 190
Gly Asn Tyr Ser Cys Phe Cys Asn Pro Gly Phe Glu Ser Ser Ser Gly
195 200 205
His Leu Ser Cys Gln Gly Leu Lys Ala Ser Cys Glu Asp Ile Asp Glu
210 215 220
Cys Thr Glu Met Cys Pro Ile Asn Ser Thr Cys Thr Asn Thr Pro Gly
225 230 235 240
Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Pro Ser Ser Gly Gln
245 250 255
Leu Asn Phe Thr Asp Gln Gly Val Glu Cys Arg Asp Ile Asp Glu Cys
260 265 270
Arg Gln Asp Pro Ser Thr Cys Gly Pro Asn Ser Ile Cys Thr Asn Ala

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Glu Gly Ser Gln Lys Asp Gly Asn Phe Ser Cys Gln Arg Val Leu Phe		
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Lys Cys Lys Glu Asp Val Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys		
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Gln Glu Gly Thr Ala Val Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln		
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Ile Asn Asn Ile Phe Ser Val Leu Asp Lys Val Cys Glu Asn Lys Thr		
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Thr Val Val Ser Leu Lys Asn Thr Thr Glu Ser Phe Val Pro Val Leu		
370	375	380
Lys Gln Ile Ser Met Trp Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser		
385	390	395
Leu Ala Thr Val Phe Leu Glu Ser Val Glu Ser Met Thr Leu Ala Ser		
405	410	415
Phe Trp Lys Pro Ser Ala Asn Val Thr Pro Ala Val Arg Ala Glu Tyr		
420	425	430
Leu Asp Ile Glu Ser Lys Val Ile Asn Lys Glu Cys Ser Glu Glu Asn		
435	440	445
Val Thr Leu Asp Leu Val Ala Lys Gly Asp Lys Met Lys Ile Gly Cys		
450	455	460
Ser Thr Ile Glu Glu Ser Glu Ser Thr Glu Thr Thr Gly Val Ala Phe		
465	470	475
Val Ser Phe Val Gly Met Glu Ser Val Leu Asn Glu Arg Phe Phe Gln		
485	490	495
Asp His Gln Ala Pro Leu Thr Thr Ser Glu Ile Lys Leu Lys Met Asn		
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Ser Arg Val Val Gly Gly Ile Met Thr Gly Glu Lys Lys Asp Gly Phe		
515	520	525
Ser Asp Pro Ile Ile Tyr Thr Leu Glu Asn Val Gln Pro Lys Gln Lys		
530	535	540
Phe Glu Arg Pro Ile Cys Val Ser Trp Ser Thr Asp Val Lys Gly Gly		
545	550	555
Arg Trp Thr Ser Phe Gly Cys Val Ile Leu Glu Ala Ser Glu Thr Tyr		
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Thr Ile Cys Ser Cys Asn Gln Met Ala Asn Leu Ala Val Ile Met Ala		

580

585

590

Ser Gly Glu Leu Thr Met Asp Phe Ser Leu Tyr Ile Ile Ser His Val
 595 600 605

595

600

605

Gly Ile Ile Ile Ser Leu Val Cys Leu Val Leu Ala Ile Ala Thr Phe
610 615 620

610

615

620

Leu Leu Cys Arg Ser Ile Arg Asn His Asn Thr Tyr Leu His Leu His
625 630 635 640

Leu Cys Val Cys Leu Leu Leu Ala Lys Thr Leu Phe Leu Ala Gly Ile
645 650 655

His Lys Thr Asp Asn Lys Thr Gly Cys Ala Ile Ile Ala Gly Phe Leu
 660 665 670

His Tyr Leu Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val
675 680 685

Ile Leu Phe Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser
690 695 700

Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu
705 710 715 720

Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr
725 730 735

Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp
 740 745 750

Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu
755 760 765

Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn
..... 775 780

Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala
700 700 700 700 700 700 700 700 700 700 700 700 700 700 700

Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe
805 810 815

Gln Ile Gly Pro Val Ala Gly Val Met Ala Tyr Leu Phe Thr Ile Ile
820 825 830

Asn Ser Leu Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn
 825 840 845

Gly Gln Val Arg Glu Glu Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys
850 855 860

Pro Ser Ser Gln Ser Gln Thr Ser Arg Ile Leu Leu Ser Ser Met Pro
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1.2.2.1. The Class

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<212> PRT
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Val Asn Glu Cys Gln Asp Thr Thr Cys Pro Ala Tyr Ala Thr Cys
35 40 45
Thr Asp Thr Thr Asp Ser Tyr Tyr Cys Thr Cys Lys Arg Gly Phe Leu
50 55 60
Ser Ser Asn Gly Gln Thr Asn Phe Gln Gly Pro Gly Val Glu Cys Gln
65 70 75 80
Asp Val Asn Glu Cys Leu Gln Ser Asp Ser Pro Cys Gly Pro Asn Ser
85 90 95
Val Cys Thr Asn Ile Leu Gly Arg Ala Lys Cys Ser Cys Leu Arg Gly
100 105 110
Phe Ser Ser Ser Thr Gly Lys Asp Trp Ile Leu Gly Ser Leu Asp Asn
115 120 125
Phe Leu Cys Ala Asp Val Asp Glu Cys Leu Thr Ile Gly Ile Cys Pro
130 135 140
Lys Tyr Ser Asn Cys Ser Asn Ser Val Gly Ser Tyr Ser Cys Thr Cys
145 150 155 160
Gln Pro Gly Phe Val Leu Asn Gly Ser Ile Cys Glu Asp Glu Asp Glu
165 170 175
Cys Val Thr Arg Asp Val Cys Pro Glu His Ala Thr Cys His Asn Thr
180 185 190
Leu Gly Ser Tyr Tyr Cys Thr Cys Asn Ser Gly Leu Glu Ser Ser Gly
195 200 205
Gly Gly Pro Met Phe Gln Gly Leu Asp Glu Ser Cys Glu Asp Val Asp
210 215 220
Glu Cys Ser Arg Asn Ser Thr Leu Cys Gly Pro Thr Phe Ile Cys Ile
225 230 235 240
Asn Thr Leu Gly Ser Tyr Ser Cys Ser Cys Pro Ala Gly Phe Ser Leu
245 250 255

Pro Thr Phe Gln Ile Leu Gly His Pro Ala Asp Gly Asn Cys Thr Asp
260 265 270

Ile Asp Glu Cys Asp Asp Thr Cys Pro Leu Asn Ser Ser Cys Thr Asn
275 280 285

Thr Ile Gly Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Ser Ser
290 295 300

Asn Gly Gln Leu Asn Phe Lys Asp Leu Glu Val Thr Cys Glu Asp Ile
305 310 315 320

Asp Glu Cys Thr Gln Asp Pro Leu Gln Cys Gly Leu Asn Ser Val Cys
325 330 335

Thr Asn Val Pro Gly Ser Tyr Ile Cys Gly Cys Leu Pro Asp Phe Gln
340 345 350

Met Asp Pro Glu Gly Ser Gln Gly Tyr Gly Asn Phe Asn Cys Lys Arg
355 360 365

Ile Leu Phe Lys Cys Lys Glu Asp Leu Ile Leu Gln Ser Glu Gln Ile
370 375 380

Gln Gln Cys Gln Ala Val Gln Gly Arg Asp Leu Gly Tyr Ala Ser Phe
385 390 395 400

Cys Thr Leu Val Asn Ala Thr Phe Thr Ile Leu Asp Asn Thr Cys Glu
405 410 415

Asn Lys Ser Ala Pro Val Ser Leu Gln Ser Ala Ala Thr Ser Val Ser
420 425 430

Leu Val Leu Glu Gln Ala Thr Thr Trp Phe Glu Leu Ser Lys Glu Glu
435 440 445

Thr Ser Thr Leu Gly Thr Ile Leu Leu Glu Thr Val Glu Ser Thr Met
450 455 460

Leu Ala Ala Leu Leu Ile Pro Ser Gly Asn Ala Ser Gln Met Ile Gln
465 470 475 480

Thr Glu Tyr Leu Asp Ile Glu Ser Lys Val Ile Asn Glu Glu Cys Lys
485 490 495

Glu Asn Glu Ser Ile Asn Leu Ala Ala Arg Gly Asp Lys Met Asn Val
500 505 510

Gly Cys Phe Ile Ile Lys Glu Ser Val Ser Thr Gly Ala Pro Gly Val
515 520 525

Ala Phe Val Ser Phe Ala His Met Glu Ser Val Leu Asn Glu Arg Phe
530 535 540

Phe Glu Asp Gly Gln Ser Phe Arg Lys Leu Arg Met Asn Ser Arg Val
545 550 555 560

Val Gly Thr Val Thr Gly Glu Lys Lys Glu Asp Phe Ser Lys Pro
 565 570 575
 Ile Ile Tyr Thr Leu Gln His Ile Gln Pro Lys Gln Lys Ser Glu Arg
 580 585 590
 Pro Ile Cys Val Ser Trp Asn Thr Asp Val Glu Asp Gly Arg Trp Thr
 595 600 605
 Pro Ser Gly Cys Glu Ile Val Glu Ala Ser Glu Thr His Thr Val Cys
 610 615 620
 Ser Cys Asn Arg Met Ala Asn Leu Ala Ile Ile Met Ala Ser Gly Glu
 625 630 635 640
 Leu Thr Met Glu Phe Ser Leu Tyr Ile Ile Ser His Val Gly Thr Val
 645 650 655
 Ile Ser Leu Val Cys Leu Ala Leu Ala Ile Ala Thr Phe Leu Leu Cys
 660 665 670
 Arg Ala Val Gln Asn His Asn Thr Tyr Met His Leu His Leu Cys Val
 675 680 685
 Cys Leu Phe Leu Ala Lys Ile Leu Phe Leu Thr Gly Ile Asp Lys Thr
 690 695 700
 Asp Asn Gln Thr Ala Cys Ala Ile Ile Ala Gly Phe Leu His Tyr Leu
 705 710 715 720
 Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val Met Leu Phe
 725 730 735
 Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser Ser Arg Asn
 740 745 750
 Ile Lys Met Leu His Leu Cys Ala Phe Gly Tyr Gly Leu Pro Val Leu
 755 760 765
 Val Val Ile Ile Ser Ala Ser Val Gln Pro Arg Gly Tyr Gly Met His
 770 775 780
 Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp Ser Phe Leu
 785 790 795 800
 Gly Pro Val Cys Met Ile Ile Thr Ile Asn Ser Val Leu Leu Ala Trp
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 Thr Leu Trp Val Leu Arg Gln Lys Leu Cys Ser Val Ser Ser Glu Val
 820 825 830
 Ser Lys Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala Ile Ala Gln
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 Ile Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe Gln Ile Gly
 850 855 860

Pro Leu Ala Ser Ile Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser Leu
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Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn Arg Gln Val
885 890 895

Arg Asp Glu Tyr Lys Lys Leu Leu Thr Arg Lys Thr Asp Leu Ser Ser
900 905 910

His Ser Gln Thr Ser Gly Ile Leu Leu Ser Ser Met Pro Ser Thr Ser
915 920 925

Lys Met Gly
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<212> PRT
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35 40 45

Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp
50 55 60

Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser
65 70 75 80

Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly
85 90 95

Tyr Glu Pro Val Ser Gly Ala Lys Thr Phe Lys Asn Glu Ser Glu Asn
100 105 110

Thr Cys Gln Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser
115 120 125

Thr Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys Arg Pro
130 135 140

Gly Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp Thr Val
145 150 155 160

Cys Glu Asp Met Thr Phe Ser Thr Trp Thr Pro Pro Pro Gly Val His
165 170 175

Ser Gln Thr Leu Ser Arg Phe Phe Asp Lys Val Gln Asp Leu Gly Arg
180 185 190

Asp Ser Lys Thr Ser Ser Ala Glu Val Thr Ile Gln Asn Val Ile Lys
195 200 205

Leu Val Asp Glu Leu Met Glu Ala Pro Gly Asp Val Glu Ala Leu Ala
210 215 220

Pro Pro Val Arg His Leu Ile Ala Thr Gln Leu Leu Ser Asn Leu Glu
225 230 235 240

Asp Ile Met Arg Ile Leu Ala Lys Ser Leu Pro Lys Gly Pro Phe Thr
245 250 255

Tyr Ile Ser Pro Ser Asn Thr Glu Leu Thr Leu Met Ile Gln Glu Arg
260 265 270

Gly Asp Lys Asn Val Thr Met Gly Gln Ser Ser Ala Arg Met Lys Leu
275 280 285

Asn Trp Ala Val Ala Ala Gly Ala Glu Asp Pro Gly Pro Ala Val Ala
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Gly Ile Leu Ser Ile Gln Asn Met Thr Thr Leu Leu Ala Asn Ala Ser
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Leu Asn Leu His Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu
325 330 335

Ser Ser Ile Arg Gly Val Gln Leu Arg Arg Leu Ser Ala Val Asn Ser
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Ile Phe Leu Ser His Asn Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu
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Phe Ala Phe Ser His Leu Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp
370 375 380

Pro Pro Ala Lys Asp Val Met Pro Gly Pro Arg Gln Glu Leu Leu Cys
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Ala Phe Trp Lys Ser Asp Ser Asp Arg Gly Gly His Trp Ala Thr Glu
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Val Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys
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Ser His Leu Ser Ser Phe Thr Ile Leu Met Ala His Tyr Asp Val Glu
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Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile
465 470 475 480

Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe
485 490 495

Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln
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Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu
545 550 555 560

Cys Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala
565 570 575

Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp
580 585 590

Phe Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile
595 600 605

Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr
610 615 620

Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala
625 630 635 640

Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys
645 650 655

Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu
660 665 670

Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr
675 680 685

Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys
690 695 700

Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser
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Thr Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser
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Glu Ser Gly Ile
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